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(54) Title: LINKED LINEAR AMPLIFICATION OF NUCLEIC ACIDS (57) Abstract The extensive synthesis ("amplification") of a nucleic acid sequence of interest is attained through a linked series of multi-cycle primer extension reactions (LLA). The primers used in each of the primer extension reactions of the process contain non-replicable elements that halt nucleic acid synthesis and thereby prevent the synthesized molecules from serving as templates in subsequent cycles. Synthesized molecules accumulate during primer extension in a mathematically linear fashion, thereby rendering the process relatively insensitive to contaminating nucleic acids. Multiple primer sets are employed, thereby ensuring the accumulation of a large number of copies of the nucleic acid sequence of interest. The invention also provides for the detection of an amplified nucleic acid sequence of interest, as well as reagent kits for carrying out the reaction.		

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LINKED LINEAR AMPLIFICATION OF NUCLEIC ACIDS
BACKGROUND OF THE INVENTION

1. Technical Field

5 The present invention relates to the in vitro
replication of nucleic acids. More specifically, the
invention relates to a process for replicating a
nucleic acid sequence of interest, with large
quantities of the desired sequence ultimately resulting
from the linkage of primer extension reactions wherein
10 the sequence of interest accumulates in a
mathematically linear fashion.

2. Brief Description of the Background Art

15 The extensive replication of nucleic acids, today
known as (and referred to herein as) nucleic acid
"amplification," finds wide utility, both practical and
theoretical, in a variety of contexts. H.G. Khorana
and his co-workers first proposed the use of an in
vitro DNA amplification process to increase available
amounts of double-stranded DNA (partial sequences of
20 the gene for the major yeast alanine t-RNA) that had
been created by the enzymatic ligation of synthetic
DNA's. See K. Kleppe et al.; J. Mol. Biol. 56:341-361
(1971). Later, in vitro amplification was applied to
the amplification of genomic DNA (Saiki et al., Science
25 230:1350-1354 (1985)) as the technique now known as the
polymerase chain reaction or "PCR." Through the wide
availability of synthetic oligonucleotide primers,
thermostable DNA polymerases and automated temperature

cycling apparatus, PCR became a widely-utilized tool of the molecular biologist.

5 The PCR process is referred to in the literature as an "exponential amplification" process. In each round or "cycle" of primer extension, a primer binding site for the other primer is synthesized. Thus, each of the synthetic DNA molecules produced in any of the previous cycles is available to serve as a template for primer-dependent replication. This aspect of the process, coupled with the presence of a sufficiently large number of primer molecules, results in synthetic DNA accumulating in a mathematically exponential manner as the reaction proceeds.

10 Although PCR has proven to be a valuable technique for the molecular biologist, and has been used extensively in the fields of human genetic research, diagnostics and forensic science, and even in the detection of antibodies, disadvantages nevertheless have been recognized. The PCR process can be difficult to quantify accurately, mainly because the amplification products increase exponentially with each round. The products of PCR, namely, double-stranded DNA molecules, are difficult to analyze or sequence per se. Strand separation typically must be carried out prior to sequencing or other downstream processes that requires single strandedness, such as hybridization to a probe capable of detecting the sequence of interest.

20 The PCR process also has proven to be quite susceptible to contamination generated through the transfer of previously amplified DNA sequences into a new reaction. This problem appears to be caused by the facts that (1) very large amounts of DNA are generated in any given reaction cycle and (2) the process uses all product DNA strands as templates in subsequent

30

cycles. Even minute quantities of contaminating DNA can be exponentially amplified and lead to erroneous results. See Kwok and Higuchi, Nature 339:237-238 (1989). Various methods to reduce such contamination have been reported in the literature (e.g. chemical decontamination, physical treatment, enzyme treatment and utilizing closed systems), as these contamination problems are widely recognized. See, John B. Findlay, "Development of PCR for in vitro Diagnostics," presented at "Genetic Recognition," Nov. 20, 1992, San Diego, CA.

There has remained a need for new nucleic acid (DNA) amplification methods that provide large amounts of DNA, and that selectively amplify only a specific sequence of interest, but which avoid the problems now associated with the "PCR" reaction. Specifically, there has remained a need for nucleic acid amplification methods that ultimately produce large amounts of a nucleic acid molecule of interest, or large amounts of a molecule containing a nucleic acid sequence of interest, but are relatively insensitive to the presence of contaminating nucleic acids. There has also remained a need for nucleic acid amplification methods that generate single-stranded products.

SUMMARY OF THE INVENTION

The foregoing and other needs are met by the present invention, which in one aspect provides a process for amplifying a specific nucleic acid sequence of interest within complementary nucleic acid strands contained in a sample, the process including the steps of:

(a) contacting the strands with a primer that contains a non-replicable element, under conditions

such that first generation primer extension products are synthesized using said strands as templates, and wherein the primer for a strand is selected such that a first generation primer extension product synthesized thereon, when separated from the strand, can serve as a template for synthesis of a second generation primer extension product of the primer for the complement of the strand;

(b) separating the first generation primer extension products from their templates to produce single-stranded molecules; and

(c) treating the first generation primer extension products with the primers of step (a) under conditions such that second generation primer extension products are synthesized using the first generation primer extension products as templates;

wherein the second generation primer extension products contain at least a portion of the nucleic acid sequence of interest and cannot serve as templates for the synthesis of extension products of the primers which were extended to synthesize their templates.

In other aspects of the invention, the products of step (c) are separated to produce single-stranded molecules, and the entire process is repeated at least once. Step (c) preferably is repeated many times, with the process being carried out in an automated fashion under the control of a programmable thermal cycling apparatus.

Following the accumulation of second generation primer extension products, each of which is incapable of serving as a template for the primer extended to prepare its first generation template, a new set of primers that contain non-replicable elements can be employed. The new set of primers advantageously bind

to the second generation synthetic products, bounding the sequence of interest to be amplified. The linear replication process is again carried out through a number of cycles. Such "linking together" of multi-cycle primer extension reactions ultimately results in thousand-fold or million-fold amplification of the original nucleic acid sequence of interest. Thus, the present process is deemed "linked linear amplification" or "LLA."

In another aspect of the invention, multiple (nested) sets of primers containing non-replicable elements can be provided in a single amplification reaction mixture. The sets are selected so as to be capable of binding to their respective templates under decreasingly stringent conditions. Thus, all the components necessary to carry out several linked linear amplifications can be provided in a single reaction mixture.

In yet another aspect of the invention, allele-specific nucleic acid replication is carried out according to the present invention with the use of primers directed to specific polymorphic sites on the template that are known to be indicative of a genetic disease or disorder, such as sickle cell disease. The allele-specific primers, containing non-replicable elements, are designed so that they prime nucleic acid synthesis of only those templates containing the desired allele.

The synthetic nucleic acid molecules resulting from the present process can be used in the diagnosis of genetic disorders or diseases, as reagents in further techniques such as gene cloning, for forensic identification, etc.

The process described herein also can be carried out using a single nucleic acid strand as a starting material. Such a process comprises:

- 5 (a) contacting the strand with a first primer containing a non-replicable element; under conditions such that a first generation primer extension product is synthesized using the strand as a template;
- (b) separating the first generation primer extension product from its template to produce single
10 stranded molecules; and
- (c) contacting the first generation primer extension product with a second primer containing a non-replicable element under conditions such that a
15 second generation primer extension product is synthesized using the first generation primer extension product as a template;

wherein the primers are selected so that the second generation primer extension product cannot serve as a template for extension of the first primer. Steps
20 (a) - (c) can be repeated many times, resulting in extensive nucleic acid synthesis, following which the reaction is linked to a subsequent reaction using a new set of primers.

The present invention also relates to a reagent
25 kit for use in amplifying a particular nucleic acid sequence. Such kit includes, for example, a DNA polymerase, a pair of primers for each sequence to be amplified wherein each of said primers comprises a non-replicable element, and, optionally, a control nucleic
30 acid sequence capable of being replicated by the primers and DNA polymerase. The kit also may contain a nucleic acid probe capable of indicating the presence or absence of an amplification product of the particular sequence.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1 - 4 comprise a schematic representation of a nucleic acid amplification process of the present invention.

5 Figures 5 - 6 comprise a schematic representation of a nucleic acid amplification process that has been linked to the process represented by Figures 1 - 4.

10 Figure 7 is a more detailed schematic representation of a nucleic acid amplification process carried out with two primers according to the present invention.

15 Figures 8 - 10 present a detailed schematic representation of a linked linear nucleic acid amplification process carried out with four primers according to the present invention.

 Figure 11 is a schematic representation of nucleic acid molecules prepared by the PCR process and by a process according to the present invention.

20 Figure 12 is a schematic representation of the sequence of the human β -globin gene (GenBank locus HUMHBB) and of several primers described herein.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

25 The nucleic acid replication process of the present invention is capable of producing large quantities of a specific nucleic acid sequence of interest. The process in its preferred form comprises a linked series of multi-cycle primer extension reactions. In each of the multi-cycle primer extension reactions, primer-dependent nucleic acid replication is
30 carried out through a number of cycles, with the primer extension products accumulating in a numerically linear fashion from cycle to cycle. A unique primer, or set

of primers, is provided for each nucleic acid strand in the starting sample that contains the sequence to be amplified. The linear accumulation of primer extension products from cycle to cycle is assured through the use of primers that contain non-replicable elements -- elements that halt the primer extension reaction, preventing the nucleic acid polymerase from replicating the entire sequence of the primer. Through the selection of appropriate primers containing such non-replicable elements, and appropriate primer annealing conditions, it is ensured that the primer extension products which accumulate in greatest abundance (referred to herein as "second generation primer extension products") cannot serve as templates themselves in subsequent cycles of primer extension using the same primers. Thus, unlike nucleic acid amplification processes (such as "PCR") which utilize the primer extension products from each cycle as templates for subsequent cycles, "exponential amplification" does not occur from cycle to cycle.

The process of the present invention utilizes and takes advantage of a number of important properties of oligonucleotide hybridization and the primer extension reaction. The invention takes advantage of the facts that:

- DNA polymerase is able to copy a template DNA many times by sequential cycles of denaturation and primer-dependent elongation.
- Primer-dependent elongation can occur, under appropriate conditions, even if the primer is not completely complementary to the template.
- Primer extension can utilize a template produced in a previous round of primer extension.

- Primer extension is inhibited by abasic sites or by non-nucleotide residues when such are present in the template nucleic acid.

5 • Primer length and composition affect, in known ways, the conditions (e.g., temperature) at which a primer will "prime" polymerase-induced extension on a template.

10 • Primer extension reactions can be performed in rapid cycles with the aid of thermal cycling apparatus.

15 The present process advantageously utilizes a series of linear amplification reactions, which can be carried out (linked) either in series or in parallel (i.e., simultaneously) to generate a very large number of copies of a nucleic acid sequence of interest. The
20 nucleic acid sequence of interest may encompass essentially the entire length of the template strand(s), or it may comprise only a very minor portion of it. The template strand(s) containing the sequence of interest may be present in a substantially
25 homogeneous sample or as part (even an extremely minor part) of a mixture of nucleic acids.

30 In accordance with the present invention, a primer that contains a non-replicable element is provided for each strand containing a sequence to be amplified. In
25 the case of a double-stranded template, the primer(s) are added either prior to or following denaturation of the template. The primers are permitted to anneal to their respective starting templates, and are extended in the presence of a polymerase enzyme, under
30 conditions appropriate for the function of the enzyme, to form first generation primer extension products. The process is repeated by denaturing the resulting duplexed nucleic acid, permitting the primers to anneal to the strands and again carrying out the primer

extension reaction. Primer extension upon the first generation primer extension products yields second generation primer extension products which, due to the presence of non-replicable elements, cannot serve as
5 templates for those same primers in subsequent cycles.

Figures 1 - 5 present a schematic representation of one series of primer extension reactions (i.e., one linear amplification reaction) carried out on a DNA template according to the process of the present
10 invention. The process is illustrated starting in step (a) with a double-stranded DNA molecule having defined termini. The strands of the starting DNA are denoted by solid (——) lines throughout Figures 1 - 4.

The starting duplex is denatured, preferably by
15 heating in a buffer solution containing the same, and the resulting single strands are contacted with a pair of primers (step (b)). Each primer preferably is provided in substantial molar excess of the starting template strand and contains within its sequence a non-
20 replicable element, here denoted by (x) or (o) within the primer sequence. Under appropriate conditions, the primers anneal to their respective templates and are elongated (step (c)) according to the primer extension reaction in the presence of a DNA polymerase and the
25 four deoxyribonucleotides. Synthesized DNA is denoted by dotted (.....) lines in Figure 1 - 4, and the DNA synthesized using the starting duplex DNA as a template is denoted "first generation" DNA. The resulting templates again are denatured, and the primers are
30 annealed (step (d)).

As seen in step (e) of Figure 2, primer elongation using first generation DNA as a template results in the preparation of second generation DNA and does not progress past the non-replicable element incorporated

into the first generation synthetic DNA. Thus, DNA molecules denoted by reference numerals 10 and 20 are synthesized. These second generation molecules do not participate further in the primer extension reaction because, as seen in the Figures, molecule 10 has not incorporated an effective binding site for the primer containing non-replicable element (x), and molecule 20 has not incorporated an effective binding site for the primer containing non-replicable element (o). Thus, as seen in steps (f) and (g), second generation molecules accumulate in a mathematically linear fashion in subsequent rounds of primer extension.

Following a desired number of cycles, the synthetic DNA is utilized as a starting material for (i.e., linked to) a second series of primer extension reactions using a second set of primers. As seen in Figures 5 - 6, primers containing non-replicable elements designated (a) and (b) are selected so as to be able to utilize molecules 10 and 20, the products of the reaction of Figures 1 - 4, as templates for further DNA synthesis. This series of primer extension reactions similarly results in the accumulation of synthetic DNA molecules, designated by reference numerals 30 and 40 in step (e) of Figure 6, which cannot serve as templates for the primers utilized in those reactions. Following a desired number of cycles, these synthetic molecules can be linked to further replication using appropriate primers again containing non-replicable elements.

It should thus be apparent that the synthetic nucleic acid products of any one series of cycles can themselves serve as templates for further amplification only if a new primer or set of primers is provided. Thus, if a first linear amplification is performed for

one hundred cycles, the one hundred copies produced from this reaction can be used as a template in a linked linear amplification (LLA) reaction using a new set of primers capable of hybridizing to the synthetic templates. One hundred additional cycles of linear amplification provides a cumulative amplification of ten thousand ($100 \cdot 100$). Repeating the process with a third set of primers yields a cumulative amplification of 1×10^6 . Additional amplification is achieved through the use of additional primers and additional cycles of primer extension.

Figure 7 schematically illustrates, in greater detail, the use of two primers in an amplification process according to the present invention. With reference to the figure, two primers are utilized for sequential rounds of primer extension. Each primer is complementary to the target sequence but contains a single non-replicable element (X) in place of one of the complementary nucleotides.

There are four reactions to consider. In reaction 1, primer P1 produces copies (first generation nucleic acid; product I) of the upper strand of the template. One copy of product I is produced during each cycle, m cycles leading to m copies. In reaction 2, primer P2 similarly produces copies (first generation nucleic acid; product II) of the lower strand of the template. One copy of product II is produced during each cycle, n cycles leading to n copies. In practice, n and m typically are the same.

In reaction 3, primer P1 produces copies (second generation nucleic acid; product III) of product II (designated template II) from reaction 2, except that template II is not replicated beyond the non-replicable

element incorporated therein. Thus, product III is not a template for either primer P1 or P2.

5 Similarly, in reaction 4, primer P2 produces copies (second generation nucleic acid; product IV) of template I, except that template I is not replicated beyond the non-replicable element. Thus, product IV is not a template for either primer P1 or P2.

10 Table 1 shows the accumulation of each product as a function of cycle number. As can be seen, the equation $(n^2+n)/2$ can be used to calculate the yield of the reaction.

Table 1: Accumulation of Products
In a Two Primer LLA Reaction

CYCLE(n)	I	cumulative I	III	cumulative III	cumulative I+III	$(n^2+n)/2$
1	1	1	0	0	1	1
2	1	2	1	1	3	3
3	1	3	2	3	6	6
4	1	4	3	6	10	10
5	1	5	4	10	15	15
6	1	6	5	15	21	21
7	1	7	6	21	28	28
8	1	8	7	28	36	36
9	1	9	8	36	45	45
10	1	10	9	45	55	55
11	1	11	10	55	66	66
12	1	12	11	66	78	78
13	1	13	12	78	91	91
14	1	14	13	91	105	105
15	1	15	14	105	120	120
100	1	100	99			5,050
200	1	200	199			20,100
500	1	500	499			125,250
1,000	1	1,000	999			500,500

If a third primer containing a non-replicable element and complementary to either product III or product IV is included in the reaction, a new product, shorter than either product III or product IV will accumulate. This product will be in greater abundance than any other DNA strand in the reaction and will remain mostly single stranded.

A reaction according to the present invention and "linking" linear amplification reactions together, to result in extensive DNA synthesis, is illustrated in Figures 8 - 10. Four primers are used in this reaction, thereby linking two two-primer reactions that are simultaneously carried out. In this reaction, primers P1 and P3 are complementary to the upper strand of the target nucleic acid and P2 and P4 are complementary to the lower strand. The complementary site for primer P3 is 5' (with respect to the template)

of the P1 complementary site. Similarly, the complementary site for primer P4 is 5' (with respect to the template) of the P2 complementary site. The nucleic acid sequence of interest advantageously will be located within the region bounded by both primer pairs.

Six different reactions can be considered, each differing in the templates used, and are shown in the figures. Reactions 1A, 1B, 2A and 2B each result in the linear accumulation of first generation synthetic nucleic acid (products 1A, 1B, 1IA and 1IB, respectively) complementary to a respective strand of the starting nucleic acid template. Reactions 3A, 3B, 4A and 4B each result in the linear accumulation of second generation synthetic nucleic acid which, due to the presence of the non-replicable element in the nucleic acid synthesized in reactions 1A, 1B, 2A and 2B, does not serve as a template for primer P1 or P2. As seen in reactions 5 and 6, however, primers P3 and P4, due to the location of their complementary site, can function to prime DNA synthesis on both original template DNA and templates IVA and IIIA, respectively. Products IIIB and IVB, of course, are not templates for any primers of this reaction, but contain the nucleic acid sequence of interest.

It will be apparent that variations to the reactions described herein will be possible. For example, the linear amplification reactions can be sequentially linked, rather than being carried out simultaneously as described in connection with Figures 8 - 10. Thus, primers P3 and P4 can be added to the reaction mixture following n cycles of primer extension, where n ranges, for example, from 2 to 100.

In another variation, primers P1 and P2 are selected so that they are capable of annealing to the template DNA and priming DNA synthesis under conditions (e.g., temperature) that do not permit primers P3 and P4 to prime. Primers P1, P2, P3 and P4 will be provided in the initial reaction mixture. The first linear amplification is carried out under the more stringent conditions, where only primers P1 and P2 participate in primer extension. Following a desired number of cycles, the reaction conditions are made less stringent, whereupon all four primers participate in nucleic acid synthesis. Primers P1 and P2 continue to generate first generation primer extension products using the starting template and second generation primer extension products using the first generation products as template; primers P3 and P4 also utilize second generation primer extension products of primers P1 and P2 as templates. Again, the nucleic acid sequence of interest advantageously is located within the region of the template strand bounded by both primer pairs.

If a fifth primer containing a nonreplicable element and complementary to either product IIIB or product IVB is included in the reaction, a new product, shorter than either IIIB or IVB, will accumulate. This product will be in greater abundance than any other DNA strand in the reaction and will remain mostly single stranded. Those skilled in the field of molecular biology will realize that whenever an odd number of primers is utilized to practice this invention, an accumulation of single stranded DNA will result.

The use of primers that contain non-replicable elements ensures that, except for primer extension products synthesized on an original template nucleic

acid strand present in the starting material (such primer extension products being referred to herein as "first generation primer extension products"), none of the synthetic nucleic acids produced during the process will serve as templates in subsequent rounds of primer extension. Thus, the accumulation of synthetic nucleic acid in a mathematically exponential manner from cycle to cycle, as achieved in the context of the PCR reaction (Kleppe et al. and Saiki et al., supra), is avoided.

Scientists experienced in the field of molecular biology and DNA chemistry will be able to synthesize primers that contain non-replicable elements. For example, primers that contain a residue of 1,3-propane diol (which halts the synthesis of DNA) can be synthesized according to the method described in Seela et al., *Nucleic Acids Res.* 15, 3113-3129 (1987) and are commercially available from Glen Research, 44901 Falcon Place, Sterling, VA, 20166 USA. Primers containing a residue of 1,4-anhydro-2-deoxy-D-ribitol, the model for the abasic site, can be synthesized with the assistance of Eritja et al., *Nucleosides & Nucleotides* 6, 803-814 (1987). Published European Patent Application 416,817 A2 (Imperial Chemical Industries PLC; March 13, 1991) describes the synthesis of primers containing one or more 2'-deoxyribofuranosyl naphthalene moieties as non-replicable elements between a primer sequence and a polynucleotide tail. The synthesis of oligonucleotide primers that contain other elements that halt polymerase-dependent copying of the template, such as derivatives of ribonucleosides and deoxyribonucleosides, will be apparent to those who are experienced in this field. The non-replicable element

preferably is not located at the terminal residue of any of the primers.

By way of example, a typical amplification reaction will be carried out starting with a double-stranded DNA molecule that contains a sequence to be replicated embedded within a much longer sequence. An oligonucleotide primer specific for each of the strands is annealed to its respective strand, with each primer containing a non-replicable element as described herein. The primers are selected so that they bind to the respective strands at positions bounding the sequence to be amplified.

A first cycle of primer extension is carried out in the presence of a DNA polymerase and the four deoxyribonucleotide bases, under conditions appropriate for the selected enzyme. The resulting first generation synthetic DNA will have incorporated therein the oligonucleotide primer at its 3' end and the entire binding site for the other primer downstream (5') therefrom.

A second cycle of primer extension is carried out, wherein the first generation synthetic DNA serves as a template for the other primer, that is, the primer which is not incorporated at its 3' end. DNA synthesis progresses along the template, but halts when the non-replicable element embedded in the template is encountered by the polymerase molecule. The resulting synthetic DNA, herein termed "second generation synthetic DNA," has discrete ends defined at its 5' end by the entire sequence of its primer, and defined at its 3' end by only a portion of the sequence of the other primer -- the portion that was copied by the DNA polymerase prior to encountering the non-replicable element.

Second generation synthetic DNA will not participate as a template for further DNA synthesis. As mentioned above, second generation synthetic DNA contains only a portion of the necessary primer binding site. Under the selected primer annealing and extension conditions, that portion of the primer binding site is insufficient to permit the primer to bind and serve as a site for primer-dependent DNA synthesis. Thus, when the third and subsequent cycles of primer extension are carried out, only original template DNA and first generation synthetic DNA participate as templates. The continued copying of those templates results in the round-to-round "linear" accumulation of second generation synthetic DNA containing the sequence of interest.

Following a desired number of primer extension cycles, additional replication can be attained by providing a second primer for each strand, the second primer(s) being selected so as to bind to regions of the original template strands within the region bounded by the original set of primers. The second primers, too, will contain non-replicable elements, thereby ensuring that their primer extension products cannot serve as templates for nucleic acid synthesis in subsequent rounds using those same primers.

It is known that primer binding conditions, especially temperature, can dictate whether a specific primer will bind to a specific template. See Rychlik et al., *Nucleic Acids Res.* 18, 6409-6412 (1990); Wu et al., *DNA Cell Biol.* 10, 233-238 (1991). Thus, in a reaction mixture containing primers of various base composition and/or lengths, the selection of a primer binding temperature can also function to select which primers will be capable of priming DNA synthesis. For

example, by providing first, second and third sets of primers that will prime at 72°, 62° and 52° C, respectively, in a single amplification reaction mixture, carrying out a first series of primer extension reactions at 72° C will ensure that only the first primer set will function to bring about primer-dependent nucleic acid synthesis. Following a desired number of cycles, the primer extension temperature can be lowered to 62° C, whereupon the first and second primer sets will prime DNA synthesis. Lowering the primer extension reaction temperature to 52° C permits all three primer sets to participate in primer-dependent DNA synthesis. The use of mixtures of primers in the present process permits the process to be carried out in an efficient manner, without the need for the researcher separately to add each primer set as the process progresses.

Through the use of available, programmable thermal cycling apparatus, all three primer sets as described above can be provided in a single amplification reaction mixture. The primers will be selected so that those that prime DNA synthesis under the most stringent conditions bind to the template 3' of the other primers. Similarly, those primers which prime under the least stringent conditions bind to the template 5' of the other primers. A first series of primer extension reactions (cycles) are carried out under the most stringent (highest temperature) primer annealing conditions, whereupon only the first set of primers participate in the synthesis of DNA containing the sequence of interest. Following a pre-selected number of primer extension cycles, the primer annealing conditions are made less stringent. The second set of primers will initiate further DNA amplification by

priming the linear copying of the second generation synthetic DNA produced during the first series of primer extension cycles under the selected conditions. When the conditions are further adjusted so that the third set of primers can participate in primer-dependent DNA synthesis, the second generation synthetic DNA's produced in both the first and second series of primer extension reactions serve as templates for DNA replication.

The design of primers that bind at preselected temperatures is within the skill of molecular biologists. The temperature at which a specific primer will function can be predicted by available algorithms (Wu et al., DNA Cell Biol. 10, 233-238 (1991)) and by computer programs (Rychlik et al., Nucleic Acids Res. 18, 6409-6412 (1990)), based upon primer length and base composition. Appropriate temperature cycling for in vitro DNA amplification can be performed manually or by commercially-available, programmable thermal cycler apparatus. Very fast cycle times can be achieved using hot air cyclers (Wittwer et al., Nucleic Acids Res. 17, 4353-4357 (1989)); cycle times as short as thirty seconds are possible (Wittwer et al., Biotechniques 10, 76-83 (1991)). Thus, one hundred cycles of primer extension can be achieved in as little as about fifty minutes.

Allele-Specific Linear Amplification

In one embodiment of the present invention, a primer is designed such that its 3' nucleotide is complementary to a particular nucleotide in the template known to be variable (polymorphic). The variable nucleotide can be a nucleotide involved in a genetic disease such as sickle cell anemia, or at

another site known to be polymorphic. If a mismatch is present between the 3' nucleotide of the primer and the corresponding nucleotide of the template DNA, the primer design insures that it will be extended poorly, or, preferably, not at all. See Petruska et al., PNAS USA 85, 6252-6256 (1988). Thus, such a primer is "allele specific" and capable of discerning the presence of absence of a single base within a nucleic acid sequence of interest. The presence of synthetic DNA following the use of an allele-specific primer in the process according to the present invention thus is indicative of the presence of the allele of interest in the original DNA template.

This allele-specific characteristic of oligonucleotide priming has been used to perform allele-specific PCR. See, for example, Newton et al., Nucleic Acids Res. 17, 2503-2516 (1989). As is the case with PCR in general, however, the exponential behavior of the allele-specific PCR reaction has been associated with difficulties in running the reaction (see Ugozzoli et al., Methods 2, 42-48 (1991)). The cycle-to-cycle linear behavior of the present amplification process, due to the presence of a non-replicable element within the allele-specific primer(s), avoids such difficulties, however.

Detection of Amplified Products

The primary products of the amplification process of the present invention are single-stranded synthetic DNA's of a defined length. The length of the product strand is determined by the position of the last-used primer and is equal to the sum of the length of the primer itself and the number of nucleotides which can be incorporated from the 3' end of the primer to the

non-replicable element of the template. The products can be detected by known nucleic acid detection techniques, including the use of primers or probes labelled with radioactivity, a fluorescent moiety or an enzyme, etc., electrophoresis, high pressure liquid chromatography, etc.

The present invention will have important application in the diagnosis of human and other animal genetic diseases. Many human genetic diseases are known to be caused by specific changes in genes of known sequence. For these specific mutations, DNA-based diagnosis is possible using hybridization or other allele specific technologies (see above) to determine which of the various gene sequences are present in the DNA of a person at risk for the disease(s). Clearly, amplification of target DNA has been very helpful in developing these technologies. The main advantages of template amplification are: smaller sample sizes can be used, the signal to noise ratio of the detection system is improved, there is a real potential for automation and the amplification system itself can be the detection system.

The processes of the present invention offer all of the same advantages offered by other amplification reactions, plus additional benefits. The products are single stranded and thus do not have to be denatured prior to detection. If an odd number of primers is used, excess single stranded molecules will be produced. These molecules will be useful, for example, as hybridization probes, and thus provide an additional advantage over other amplification technologies. Still further advantages are presented as the products accumulate linearly and thus can be accurately quantified; the occurrence of "false positives" will be

reduced in comparison with exponential processes that use newly-synthesized DNA as a template in subsequent rounds using the same primer.

EXAMPLES

- 5 Solutions utilized in several of the following examples are described below:
- TE (Tris-EDTA): 10 mM Tris-HCl, 1 mM EDTA, pH 8.0
- TBE (Tris-Borate-EDTA): 89 mM Tris-HCl, 89 mM Boric Acid, 2 mM EDTA, pH 8.3
- 10 Klenow polymerase Buffer: 50 mM Tris-HCl, 10 mM MgCl₂, pH 7.6
- Kinase Buffer: 50 mM Tris-HCl, 10 mM MgCl₂, 5 mM DTT, 0.1 mM spermidine-HCl, 0.1 mM EDTA, pH 7.6
- DNA Polymerase I buffer: 50 mM Tris-HCl, 10 mM MgSO₄, 0.1 mM DTT, 50 µg/ml bovine serum albumin, pH 7.2
- 15 Sequenase buffer: 40 mM Tris-HCl, 20 mM MgCl₂, 50 mM NaCl, pH 7.5
- Bst polymerase buffer: 20 mM Tris-HCl, 20 mM MgCl₂, pH 8.5
- 20 Thermus aquaticus polymerase buffer: 50 mM KCl, 10 mM Tris-HCl, 1.5 mM MgCl₂, 0.01% w/v gelatin, pH 8.3
- 10X Ficoll loading buffer: 100 mM Tris-HCl pH 7.5, 10 mM EDTA, 0.5% bromophenol blue, 0.5% xylene cyanol, 30% Ficoll
- 25 5X SSPE: 50 mM sodium phosphate pH 7.0, 0.9 mM NaCl and 5 mM EDTA
- 6X SSC: 0.9 M NaCl, 0.09 M sodium citrate
- The inventive process is illustrated by the following examples, which do not limit the scope of
- 30 protection sought.

Example 1 - 1,3 Propane Diol Blocks Primer
Extension When Present in a Template

5 A template with or without a single nucleotide
base containing a 1,3 propane diol moiety (designated
as non-replicable element "X") and a primer
complementary to the 3' end of the template were
synthesized in order to demonstrate the ability of the
1,3 propane diol moiety to serve as a non-replicable
element and halt DNA synthesis. The sequences
10 synthesized are as follows:

<u>Name</u>	<u>Sequence (5' - 3')</u>
DNA II 207	GCTCCCTTAGCATGGGAGAGTCTCCGGTTC
DNA II 207X	GCTCCCTTAXCATGGGAGAGTCTCCGGTTC
P12	GAACCGGAGACT

15 The primers and templates were annealed to form the
following primer template complexes:

5' GCTCCCTTAGCATGGGAGAGTCTCCGGTTC
TCAGAGGCCAAG 5'

20 5' GCTCCCTTAXCATGGGAGAGTCTCCGGTTC
TCAGAGGCCAAG 5'

The primer template complexes were then extended with
various DNA polymerases (Klenow fragment of DNA
Polymerase I, AmpliTaq polymerase (Perkin Elmer - Cetus
Corp.), BST polymerase (Bio-Rad Laboratories, Hercules,
25 CA) and Sequenase polymerase (United States
Biochemical, Cleveland, OH) in the presence of α -[32 P]-
dCTP and the products were subjected to electrophoresis
on a denaturing polyacrylamide gel.

30 The primer and templates were mixed at a
primer/template ratio of 10, and buffers appropriate
for the polymerase enzymes were employed. Twenty μ l

reactions containing 1 pmol of either 207 or 207-X, 10 pmol P12, 25 μ M dNTPs, 0.5 μ Ci of α -[32 P]-dCTP and either AmpliTaq buffer, BST buffer, Klenow buffer or Sequenase buffer. The samples were heated at 90°C for two minutes and cooled to 0°C for five minutes before adding one unit of DNA polymerase and reacting at 37°C for 10 minutes. The results indicate that the propane diol residue blocks primer elongation for all four DNA polymerases as shown below:

10 5'GCTCCCTTAGCATGGGAGAGTCTCCGGTTC
 <-----TCAGAGGCCAAG 5'

5'GCTCCCTTAXCATGGGAGAGTCTCCGGTTC
 <-----TCAGAGGCCAAG 5'

15 Example 2 - Primers With Propane Diol-Containing Base Do Not Support PCR

Four oligonucleotides were prepared, two of which contained the non-replicable 1,3-propane diol moiety. The sequences were synthesized on an Eppendorf Ecosyn D300 automated DNA synthesizer with the MMT-propane diol phosphoramidite in the 2 position. When entering the sequence into the synthesizer, a Z was introduced. The sequences are presented in the following table:

<u>Name</u>	<u>Sequence (5' - 3')</u>
BGP-2 22	GGGTGGGAAAATAGACCAATAG
25 BGP-2 22X	GGGTGGGAAAATAGACCXATAG
BGP-1 30	GGCAGGAGCCAGGGCTGGGCATAAAAGTCA
BGP-1 30X	GGCAGGAGCCAGGGCTGGGCATAAA X GTCA

The sites of complementarity of the oligonucleotides in the human β -globin gene (GenBank Locus HUMHBB) is shown in Figure 12.

In vitro amplification reactions were performed with various combinations of the four primers. Each reaction contained 100 ng of human genomic DNA, 6 pmol of each of two primers, in a standard PCR reaction buffer. Reactions were placed in a thermal cycler (Ericomp) and heated to 94°C for three minutes, cooled to 55°C for 30 seconds, heated to 72°C for 30 seconds and then subjected to 31 cycles of heating and cooling as follows: 94°C, one minute, 55°C, 30 seconds, 72°C for 30 seconds. Following thermal cycling the sample was incubated at 72°C for an additional 3.5 minutes. Only the reaction containing the primers without propane diol (BGP-1 30 and BGP-2 22) gave a 319 bp amplification product. Thus it was confirmed that the propane diol-containing primers do not support PCR.

Example 3-Propane Diol-Containing
Primers Produce Specific DNA Fragments

The plasmid pHB^A was mixed with propane diol-containing primers (BGP-1 30X and BGP-2 22X) or control primers (BGP-1 30 and BGP-2 22) not containing propane diol moieties. The primer/template mixtures were subjected to thermal cycling conditions of 94°C for 20 seconds to dissociate the double-stranded template, followed by 48°C for 20 seconds. After the final cycle, the reaction mixtures were incubated a further 5 minutes 40 seconds at 48°C to complete the primer extension reaction and anneal the single stranded DNA's. The reaction mixtures employing the propane diol-containing primers (according to the present invention) were cycled through 45 rounds of primer extension. The PCR reactions, utilizing the primers not containing propane diol moieties were cycled through 10 rounds of primer extension. The products of

the reactions were subjected to electrophoresis on 1.5% agarose (TBE buffer). The propane diol-containing primers produce a DNA fragment which was smaller than the PCR generated fragment. The smaller size is due to
5 the fact that the primer extension does not extend to the end of the template strand, leaving 5' extensions on the product.

Figure 11 presents a comparison of the products of a PCR reaction and of an LLA reaction according to the
10 present invention. The major products of a PCR reaction, which accumulate exponentially, are completely double-stranded with defined ends corresponding to the ends of the primers employed. The products of the present process, however, are shorter
15 than corresponding PCR products, as primer extension past the non-replicable element does not occur.

Example 4 - Propane Diol-Containing Primers Support DNA Amplification

An amplification reaction according to the present
20 invention was performed using BGP-1 30X and BGP-2 22X for various numbers of cycles. The products of the amplification were subjected to dot blot hybridization, and the hybridization signal was compared to that obtained from a known amount of plasmid DNA containing
25 the sequence.

Fifteen μ l reactions were prepared containing 1.1 ng of the plasmid pHB^A (containing the entire human β -globin gene cloned in pBR322), 5 pmol of BGP-1 30X, 5 pmol of BGP-2 22X, 83 μ M dNTP, 2.5 units AmpliTaq[®] DNA
30 polymerase in a standard PCR buffer. Thermal cycling reactions were performed in a Corbett Research FTS-1 thermal cycler for 45, 32 and 22 cycles with the following program: 94°C 20 seconds, 48°C 20 seconds.

At the end of the cycling the reactions were heated to 94°C for 20 seconds and then incubated at 48°C for four minutes.

The products of the reactions (3 µl) were mixed with 10 µl 4N NaOH, 250 mM EDTA and were blotted onto a Zeta-Probe membrane (Bio-Rad Laboratories, Hercules, CA). Also included on the membrane was 56, 118 and 231 ng of the plasmid pHB^A similarly denatured. The membrane was hybridized with 5'-³²P-CTGCAGTAACGGCAGACTTCTCCT at 55°C for three hours in 5X SSPE, 1% SDS, 5 mg/ml Blotto, 10 µg/ml Homomix I RNA. After hybridization the blot was washed at room temperature in 6X SSC and then scanned in a Bio-Rad Molecular Imager. The reaction produced approximately 250 fold amplification demonstrating the process of the present invention results in the amplification of the nucleic acid sequence of interest.

Example 5 - Amplification Of The Human
β-globin Gene From Genomic DNA

Linear amplification reactions were performed according to the present invention in a 15 µl volume containing Thermus aquaticus polymerase buffer, template DNA (800 ng of genomic DNA or 10⁴ molecules of plasmid pHB^A), 200 µM each dNTP (dATP, dTTP, dCTP, and dGTP), 2 pmol of oligonucleotide primers BGP5-22X and BGP4-22X, and 2 units of Ampli-Taq Polymerase (Perkin-Elmer Cetus). Plasmid pHB^A contains a 4.4 kb Pst I fragment of the human β-globin gene cloned at the Pst I site of pBR322. As a negative control, a reaction was carried out which included all the ingredients used in the previous reactions except the template DNA (a "no template" control). After denaturing the template DNA for 3 min, the amplification was performed for 99

cycles as follows: annealing at 55 °C for 30 sec,
polymerization at 72 °C for 15 sec, and denaturation at
94 °C for 30 sec. At the end of the last cycle, the
samples were annealed at 55 °C for 30 sec and finally
polymerized at 72 °C for 4 min.

At the end of the first step (100 cycles), 7.5 µl
were removed from each sample (genomic DNA, plasmid
DNA, and negative control), and mixed with 7.5 µl
containing Thermus aquaticus polymerase buffer, 5 pmol
of primers BGP1-35X and BGP2-35X, and 2 units of Ampli-
Taq Polymerase. The cycling program was similar to the
program used in the first step, except that the
annealing temperature was 63 °C.

To control the size of the fragments generated by
the amplifications, two reactions were performed. One
reaction contained Thermus aquaticus polymerase buffer,
5 pmol of primers BGP5-22X and BGP4-22X, 1 x 10⁸
molecules of plasmid pHB^A, and 3 units of Ampli-Taq
Polymerase. The second control included the same
ingredients as the previous reaction except that the
primers BGP1-35X and BGP2-35X were used. The template
DNA was denatured for 4 min at 94 °C and then cycled 48
times using the following conditions program: annealing
and polymerization at 55 °C for 30 sec; denaturation at
94 °C for 30 sec. At the end of the last cycle the
samples were annealed at 55 °C for 30 sec and
polymerized at 72 °C for 4 min.

<u>Primer</u>	<u>Sequence (5'--> 3')</u>
BGP1-35X	CCAGGGCTGGGCATAAAAGTCAGGGCAGAGXCATC
BGP2-35X	GGGTGGGAAAATAGACCAATAGGCAGAGAGXGTCA
BGP4-22X	CCAAAGGACTCAAAGAAXTCTCT
BGP5-22X	CCTCACCTGTGGAGCCXCACC

Analysis of the LLA products:

The entire reaction (15 μ l) was mixed with 1.6 μ l 10X Ficoll loading buffer and subjected to electrophoresis in a 1.5% agarose gel (Bio-Rad ultrapure agarose). Electrophoresis was performed in TBE buffer for 90 min at 110 volts. The gel was subsequently stained with ethidium bromide (1 μ g/ml) for 30 min, destained for 15 min, and photographed by ultraviolet (UV) illumination. The electrophoresed DNA was then transferred to a nylon membrane (Zeta probe, Bio-Rad) by alkaline transfer (Reed, K. C. and D. A. Mann, Rapid transfer of DNA from agarose gels to nylon membranes, Nucleic Acids Res. 13:7207-7221 (1985)) and fixed to the membrane by UV radiation (Church, G. M. and W. Gilbert, Genomic Sequencing, Proc. Natl. Acad. Sci. U. S. A. 81:1991-1995 (1984)). The membrane was prehybridized in 5X SSPE, 1% SDS, 10 μ g/ml homomix RNA and 0.5% dehydrated powdered skim milk (Carnation, Los Angeles, CA) for one hour and subsequently hybridized with 2.5×10^6 cpm/ml 5' end 32 P labeled probe 5'CAGGAGTCAGGTGCACCATGGT for two hours at 55 °C. The membrane was washed twice with 6X SSC for 30 min at room temperature and autoradiographed at room temperature for 30 min.

The genomic DNA produced the same fragment as the globin gene plasmid DNA control. The size of the fragment is that produced by the BGP1-35X and BGP2-35X primers.

Example 6: LLA Amplification Products Are Resistant To Contamination In Comparison With PCR In vitro amplifications:

The "LLA" amplification reaction of the present invention was carried out in a 15 μ l volume containing

Thermus aquaticus polymerase buffer, template DNA (3.5×10^9 molecules of plasmid pH β^A), 200 μ M each dNTP (dATP, TTP, dCTP, and dGTP), 5 picomoles of oligonucleotide primers BGP1-22X and BGP2-22X, and 1.25 units of Ampli-Taq DNA Polymerase (Perkin-Elmer Cetus). After denaturing the template DNA for 1 min, the amplification was performed for 49 cycles by annealing at 48 °C for 30 seconds and denaturing at 94 °C for 30 seconds. At the end of the last cycle, the samples were incubated at 48 °C for 4 min.

The PCR reaction was performed for comparison purposes in a 15 μ l volume containing Thermus aquaticus polymerase buffer, template DNA (3.5×10^9 molecules of plasmid pH β^A), 200 μ M each dNTP (dATP, TTP, dCTP, and dGTP), 5 picomoles of oligonucleotide primers BGP1-22 and BGP2-22, and 1.25 units of Ampli-Taq DNA Polymerase. After denaturing the template DNA for 1 min, the amplification was performed for 9 cycles by annealing at 48 °C for 30 seconds and denaturing at 94 °C for 30 seconds. At the end of the last cycle, the samples were incubated at 48 °C for 4 min.

Analysis of the LLA and PCR products

Two fold serial dilutions of the LLA and PCR products (1/64 μ l, 1/32 μ l, 1/16 μ l, 1/8 μ l, 1/4 μ l, 1/2 μ l, 1 μ l, 2 μ l, 4 μ l, and 8 μ l) were mixed with 1x Ficoll loading buffer and subjected to electrophoresis in a 1.5% agarose gel. Electrophoresis was performed in 1x TBE buffer for 90 min at 110 volts. The electrophoresed DNA was transferred to a nylon membrane by alkaline transfer (Reed and Mann, 1985), cross linked by UV radiation (Church and Gilbert, 1984), and then neutralized with 2x SSC. Subsequently, the membrane was hybridized in 5x SSPE, 1% sodium dodecyl sulfate (SDS), 10 μ g/ml homomix RNA, 0.5% powdered skim

5 milk and 2.5×10^6 cpm of the ^{32}P labelled probe
5' CAGGAGTCAGGTGCACCATGGT. The hybridization took place
at 55 °C for two hours. After hybridization, the
membrane was washed twice with 6x SSC at room
temperature for 15 min. and then scanned and quantified
with the Bio-Rad GS-250 Molecular Imager.

Amplicon contamination experiments

10 Equal amounts of LLA (1/26 μl) and PCR (1/16 μl)
products (as quantified with the imager (above)) were
diluted with distilled water by 10^4 , 10^5 , and 10^6 fold;
these dilutions were subsequently used as DNA templates
in PCR reactions. The amplification reactions were
performed in a 15 μl volume containing Thermus
15 aquaticus polymerase buffer, template DNA (LLA or PCR
dilutions), 200 μM each dNTP (dATP, TTP, dCTP and
dGTP), 5 picomoles of oligonucleotide primers BGP1-22
and BGP2-22, and 1 unit of Ampli-Taq Polymerase.
Reactions were duplicated and after a first step of
thermal denaturation for 3 min at 94 °C, the samples
20 were run for 25 and 30 cycles of amplification (30
seconds at 55 °C, 30 seconds at 72 °C, and 30 seconds
at 94 °C) and finally incubated at 50 °C for 30 seconds
and 4 min at 72 °C. Furthermore, a negative control
which contained all reagents except the template DNA
25 was included.

To control and quantify the relative amounts of
LLA and PCR DNA templates, a second PCR reaction set
was performed using a different primer set (MD040 and
PC04) which prime internally to BGP1-22 and BGP2-22.
30 The reaction ingredients (except the primers) and
reaction conditions were as described in the previous
paragraph.

The 15 μl reaction volumes were mixed with 1.6 μl
10X Ficoll loading buffer and subjected to

electrophoresis in a 1.5% agarose gel (Bio-Rad ultrapure agarose). Electrophoresis was performed in 1x TBE buffer for 90 min at 110 volts. The gel was subsequently stained with ethidium bromide (1 µg/ml) for 30 min, destained for 15 min, and photographed by ultraviolet (UV) illumination. The electrophoresed DNA was then transferred to a nylon membrane by alkaline transfer (Reed and Mann (1985)) and fixed to the membrane by UV radiation (Church (1984)). The membrane was prehybridized in 5X SSPE, 1% SDS, 10 µg/ml Homomix RNA and 0.5% dehydrated powdered skim milk for one hour and subsequently hybridized with 2.5×10^6 cpm/ml of the 5'-P³² labeled probe 5'CAGGAGTCAGGTGCACCATGGT for two hours at 55 °C. The membrane was washed twice with 6X SSC for 30 min at room temperature and the reactions were quantified with the Bio-Rad GS-250 Molecular Imager.

Results

The ratio of hybridization of reactions amplified with the outside primer set (measuring the ability of the amplicon to amplify in the second reaction) to the inside primer set (measuring the amount of amplicon present in the reaction) was determined. As can be seen from the following table, LLA reactions produce an amplicon which is very resistant to amplification from the outside primers and therefore will be resistant to the effects of carry over contamination.

Table II: Effect of Contamination
On subsequent Amplification

Dilution	Outside:Inside (PCR)	Outside:Inside (LLA)
10 ⁻⁴	1.58	0.17
10 ⁻⁵	1.62	0.02

CLAIMS

I Claim:

1. A process for amplifying a nucleic acid sequence of interest contained within complementary nucleic acid strands, comprising:

5 (a) contacting the strands with a primer that contains a non-replicable element, under conditions such that first generation primer extension products are synthesized using said strands as templates, and wherein the primer for a strand is selected such that a first generation primer extension product synthesized
10 thereon, when separated from the strand, can serve as a template for synthesis of a second generation primer extension product of the primer for the complement of said strand;

(b) separating the first generation primer
15 extension products from their respective templates to produce single-stranded molecules; and

(c) treating the first generation primer extension products with the primers of step (a) under conditions such that second generation primer extension products
20 are synthesized using the first generation primer extension products as templates;

wherein the second generation primer extension products contain at least a portion of the nucleic acid sequence of interest and cannot serve as templates for
25 the synthesis of primer extension products of the primers which were extended to synthesize their templates.

2. A process according to claim 1 further comprising separating the second generation primer
30 extension products generated from their respective templates to produce single-stranded molecules.

3. A process according to claim 1 wherein step (c) is repeated at least once.

4. A process according to claim 1 wherein the non-replicable element is not located at the terminal residue of any of said primers.

5. A process according to claim 1 wherein the non-replicable element is a derivative of a deoxyribonucleotide.

6. A process according to claim 1 wherein the non-replicable element is a derivative of a ribonucleotide.

7. A process according to claim 5 wherein the non-replicable element is a residue of 1,3-propane diol.

8. A process according to claim 5 wherein the non-replicable element is a residue of 1,4-anhydro-2-deoxy-D-ribitol.

9. A process according to claim 1 further comprising the step of treating the second generation primer extension products with primers containing a non-replicable element under conditions such that primer extension products are synthesized utilizing the second generation primer extension products as templates.

10. A process for amplifying a nucleic acid sequence of interest contained within complementary nucleic acid strands, comprising:

(a) contacting strands with first primers and second primers, each of said first and second primers containing a non-replicable element, under conditions such that a first generation primer extension product is synthesized from said first and second primers using the strands as templates, and wherein the first and second primers are selected such that the first

generation primer extension products, when separated from their templates, can serve as templates for synthesis of second generation primer extension products of the first and second primers;

15 (b) separating the first generation primer extension products from their respective templates to produce single-stranded molecules; and

(c) treating the first generation primer extension products with the first and second primers under
20 conditions such that second generation primer extension products are synthesized using the first generation primer extension products as templates;

wherein the second generation primer extension products contain at least a portion of the nucleic acid
25 sequence of interest, the second generation primer extension products of the first primers being capable of serving as templates for the production of primer extension products of the second primers.

11. A process according to claim 10 further
30 comprising separating the primer extension products generated from step (c) to produce single-stranded molecules.

12. A process according to claim 10 wherein step (c) is repeated at least once.

35 13. A process according to claim 10 wherein the non-replicable element is not located at the terminal residue of any of said primers.

14. A process according to claim 10 wherein the non-replicable element is a derivative of a
40 deoxyribonucleotide.

15. A process according to claim 10 wherein the non-replicable element is a derivative of a ribonucleotide.

45 16. A process according to claim 14 wherein the non-replicable element is a residue of 1,3-propane diol.

17. A process according to claim 14 wherein the non-replicable element is a residue of 1,4-anhydro-2-deoxy-D-ribitol.

5 18. A process according to claim 10 further comprising treating the second generation primer extension products of said second primers with third primers, each of said third primers containing a non-replicable element, under conditions such that third-primer primer extension products are formed utilizing the second generation primer extension products of said second primers as templates.

19. A process according to claim 10 wherein each of said strands contains a primer binding site for a first primer and a primer binding site for a second primer, the primer binding site for the first primer being 3' of the primer binding site for the second primer.

20. A process for amplifying a nucleic acid sequence of interest contained within complementary nucleic acid strands, comprising:

5 (a) contacting the strands with first primers and second primers, each of said first and second primers containing a non-replicable element, under a first set of primer extension reaction conditions such that first generation primer extension products are synthesized from the first primers, and not from the second
10 primers, using the strands as templates, and wherein the first primers are selected such that a first generation primer extension product from this step, when separated from its template, can serve as a template for synthesis of a second generation extension

product of the first primer for the complement of said strand;

5 (b) separating the first generation primer extension products from their respective templates to produce single-stranded molecules;

10 (c) treating the first generation primer extension products with the primers of step (a) under conditions such that second generation primer extension products are generated using first generation primer extension products as templates;

(d) separating the second generation primer extension products from their templates to produce single-stranded molecules;

(e) repeating steps (c) and (d) at least once; and

(f) subjecting the reaction mixture of step (e) to a second set of primer extension reaction conditions such that primer extension products are synthesized from said second primers using second generation primer extension products as templates.

21. A process according to claim 20 wherein said first set of primer extension reaction conditions are more stringent than said second set of primer extension reaction conditions.

22. A process according to claim 20 wherein said first set of conditions comprises a higher temperature than said second set of conditions.

23. A process according to claim 20 wherein the non-replicable element is not located at the terminal residue of any of said primers.

24. A process according to claim 20 wherein the non-replicable element is a derivative of a deoxyribonucleotide.

25. A process according to claim 20 wherein the non-replicable element is a derivative of a ribonucleotide.

26. A process according to claim 24 wherein the non-replicable element is a residue of 1,3-propane diol.

27. A process according to claim 24 wherein the non-replicable element is a residue of 1,4-anhydro-2-deoxy-D-ribitol.

28. A process according to claim 20 wherein each of said strands contains a primer binding site for a first primer and a primer binding site for a second primer, the primer binding site for the first primer being 3' of the primer binding site for the second primer.

29. A process according to claim 1 wherein the nucleic acid sequence contains a polymorphic site associated with a genetic disease, and each of said primers are selected so as to prime nucleic acid synthesis only in the presence or only in the absence of said disease state.

30. A process according to claim 29, wherein said genetic disease is sickle cell anemia.

5 31. A process according to claim 1 further comprising detecting the presence or absence of an amplified nucleic acid sequence of interest.

32. A process according to claim 10 further comprising detecting the presence or absence of an amplified nucleic acid sequence of interest.

10 33. A process according to claim 20 further comprising detecting the presence or absence of an amplified nucleic acid sequence of interest.

34. A reagent kit for use in amplifying a particular nucleic acid sequence, comprising a DNA

polymerase, a pair of primers for each sequence to be amplified wherein each of said primers comprises a non-replicable element, and a control nucleic acid sequence capable of being replicated by said primers and DNA
5 polymerase.

35. A reagent kit according to claim 34 wherein the non-replicable element is a residue of 1,3-propane diol.

10 36. A reagent kit according to claim 34 wherein the non-replicable element is a residue of 1,4-anhydro-2-deoxy-D-ribitol.

15 37. A reagent kit for use in amplifying a particular nucleic acid sequence, comprising a DNA polymerase, a pair of primers for each sequence to be amplified wherein each of said primers comprises a non-replicable element, and a nucleic acid probe capable of detecting the presence or absence of an amplification product of the particular nucleic acid sequence.

20 38. A reagent kit according to claim 37 and further comprising a control nucleic acid sequence capable of being replicated by said primers and DNA polymerase and capable of being detected by said nucleic acid probe.

25 39. A reagent kit according to claim 37 wherein the non-replicable element is a residue of 1,3-propane diol.

40. A reagent kit according to claim 37 wherein the non-replicable element is a residue of 1,4-anhydro-2-deoxy-D-ribitol.

30 41. A reagent kit according to claim 34 wherein said primers are selected so as to amplify a nucleic acid sequence indicative of a genetic disease or abnormality.

42. A reagent kit according to claim 37 wherein said primers are selected so as to amplify a nucleic acid sequence indicative of a genetic disease or abnormality.

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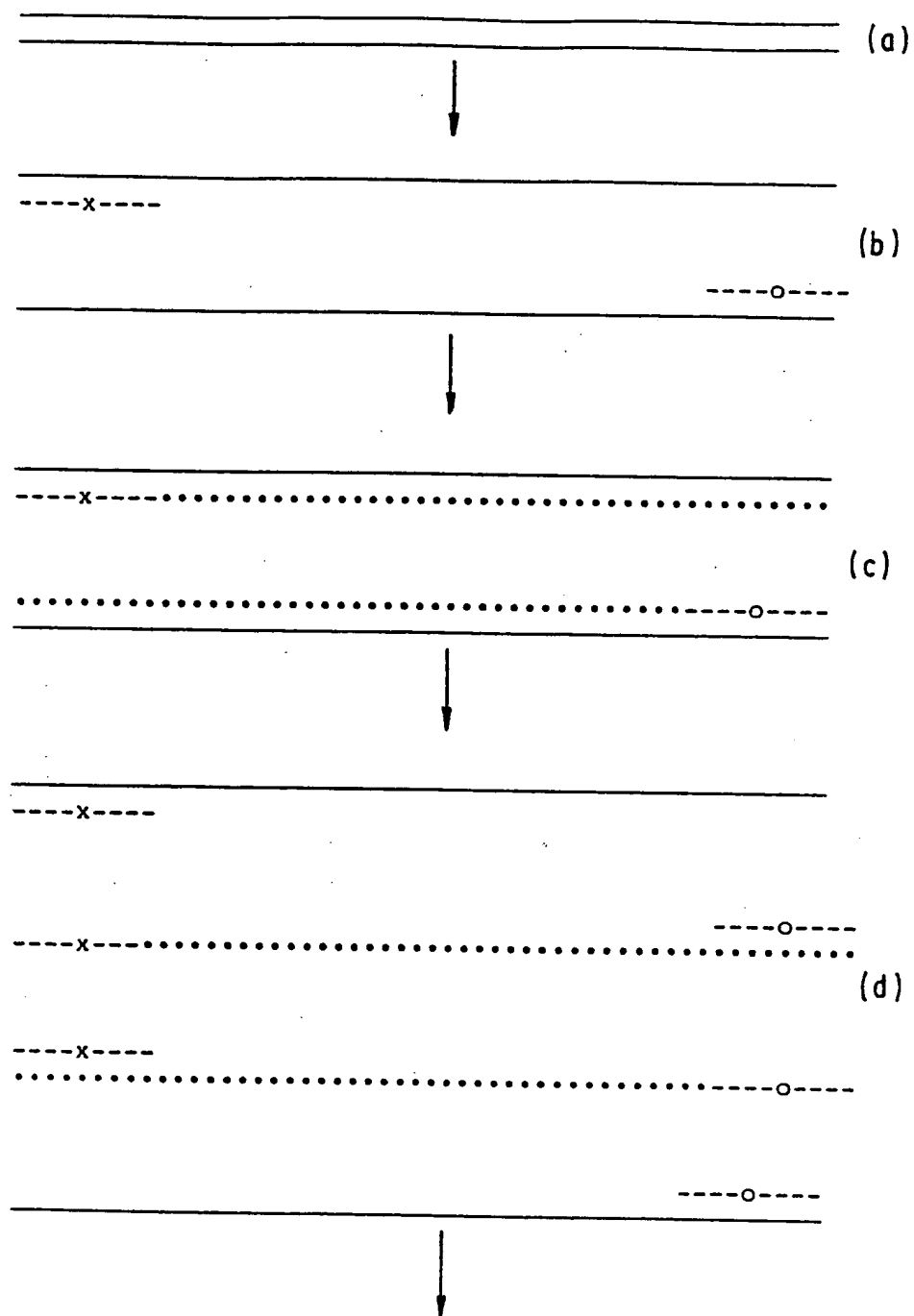


FIGURE 1
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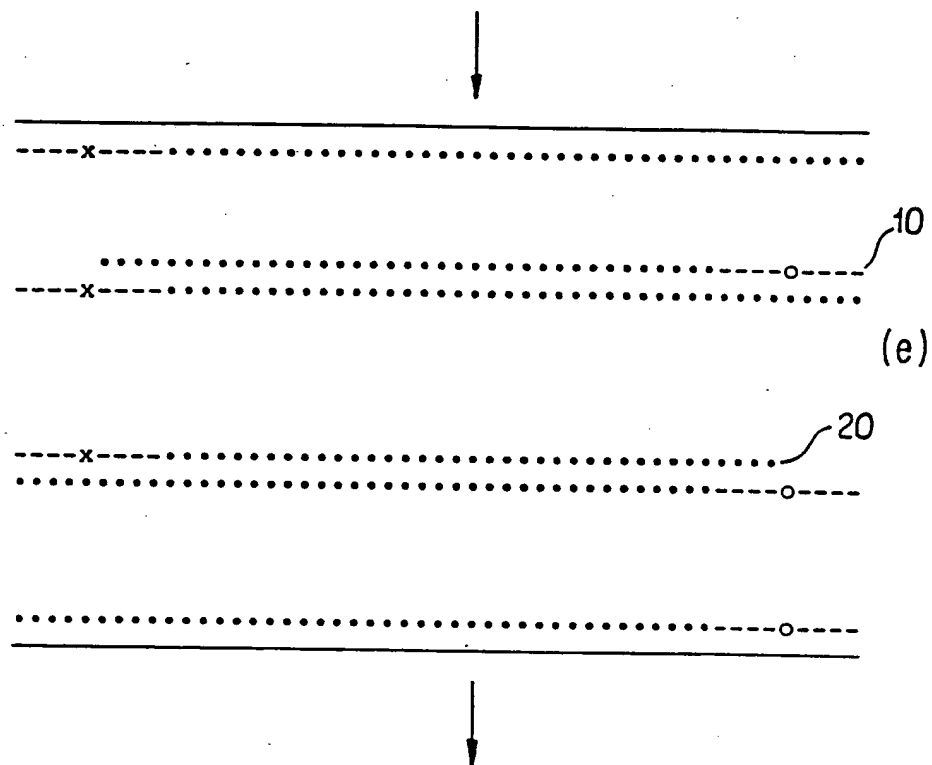


FIGURE 2

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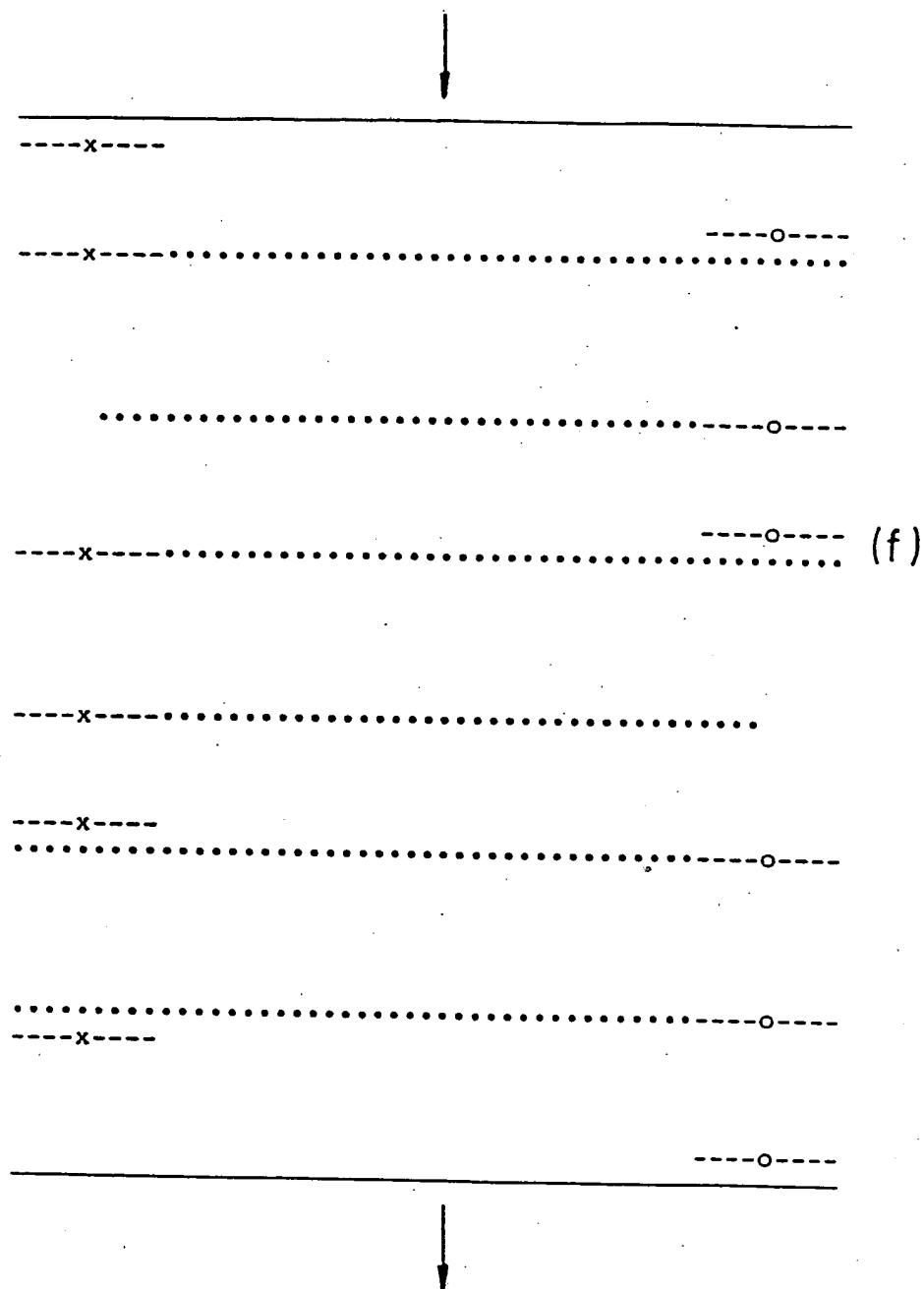
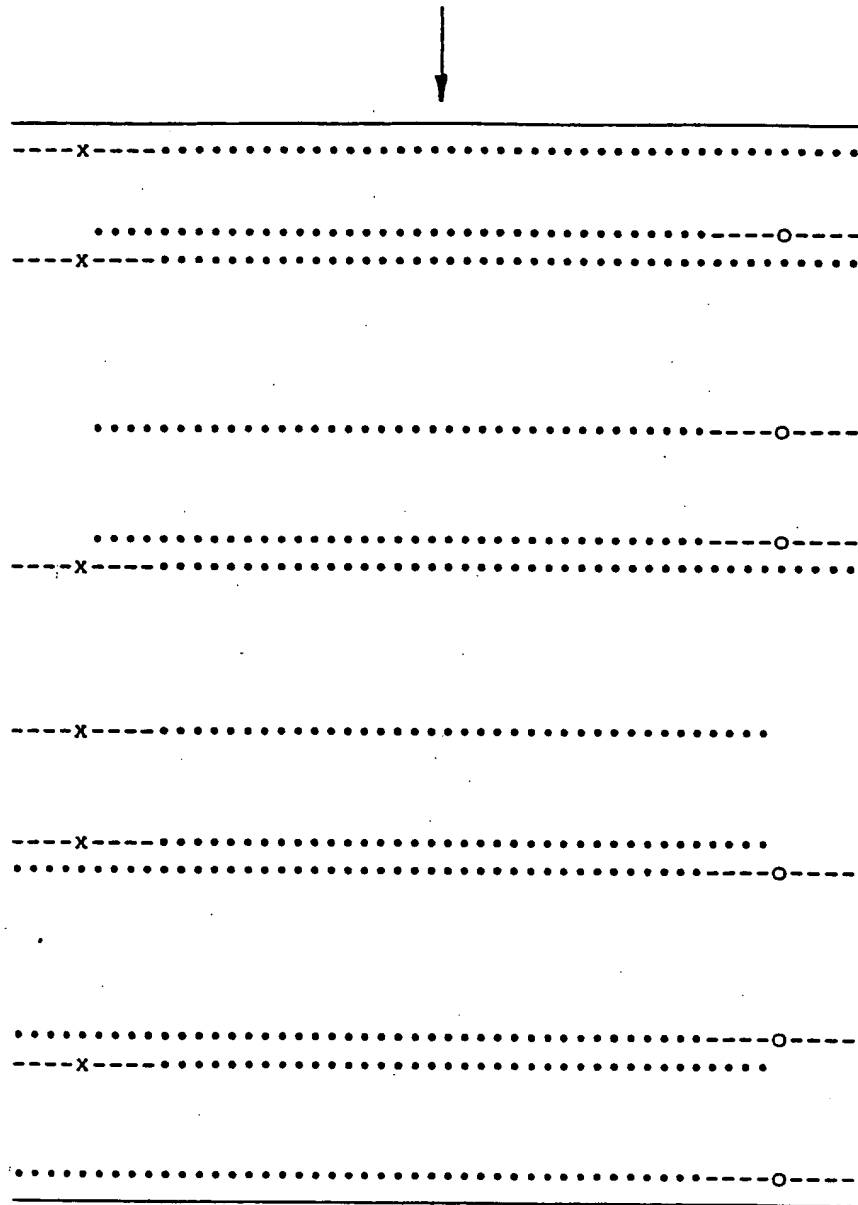


FIGURE 3

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(g)

FIGURE 4

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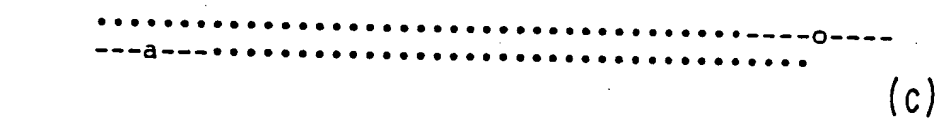
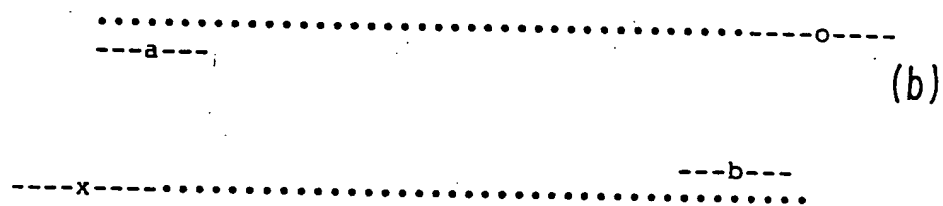
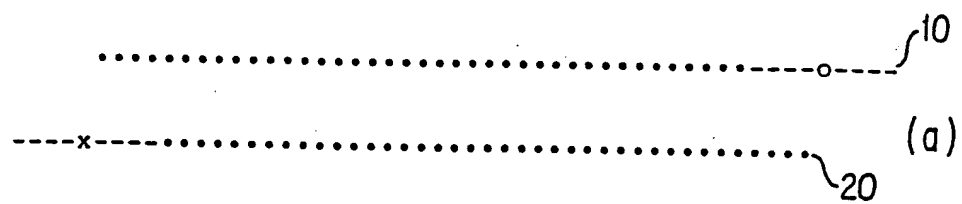


FIGURE 5

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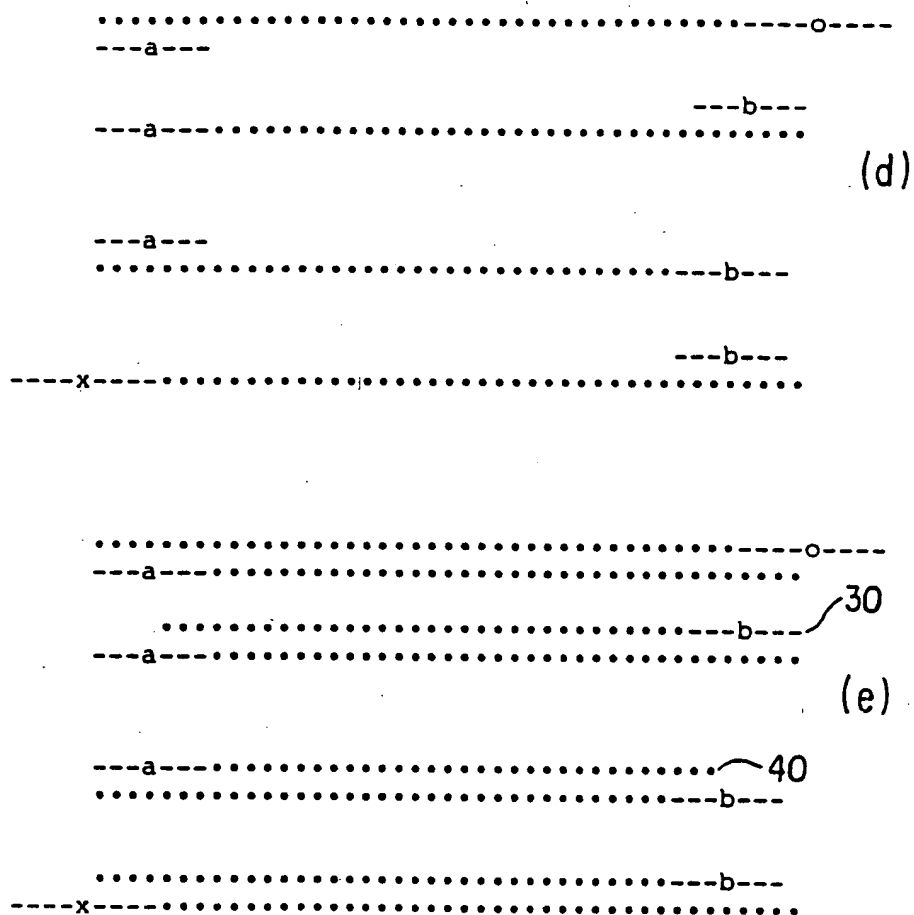


FIGURE 6

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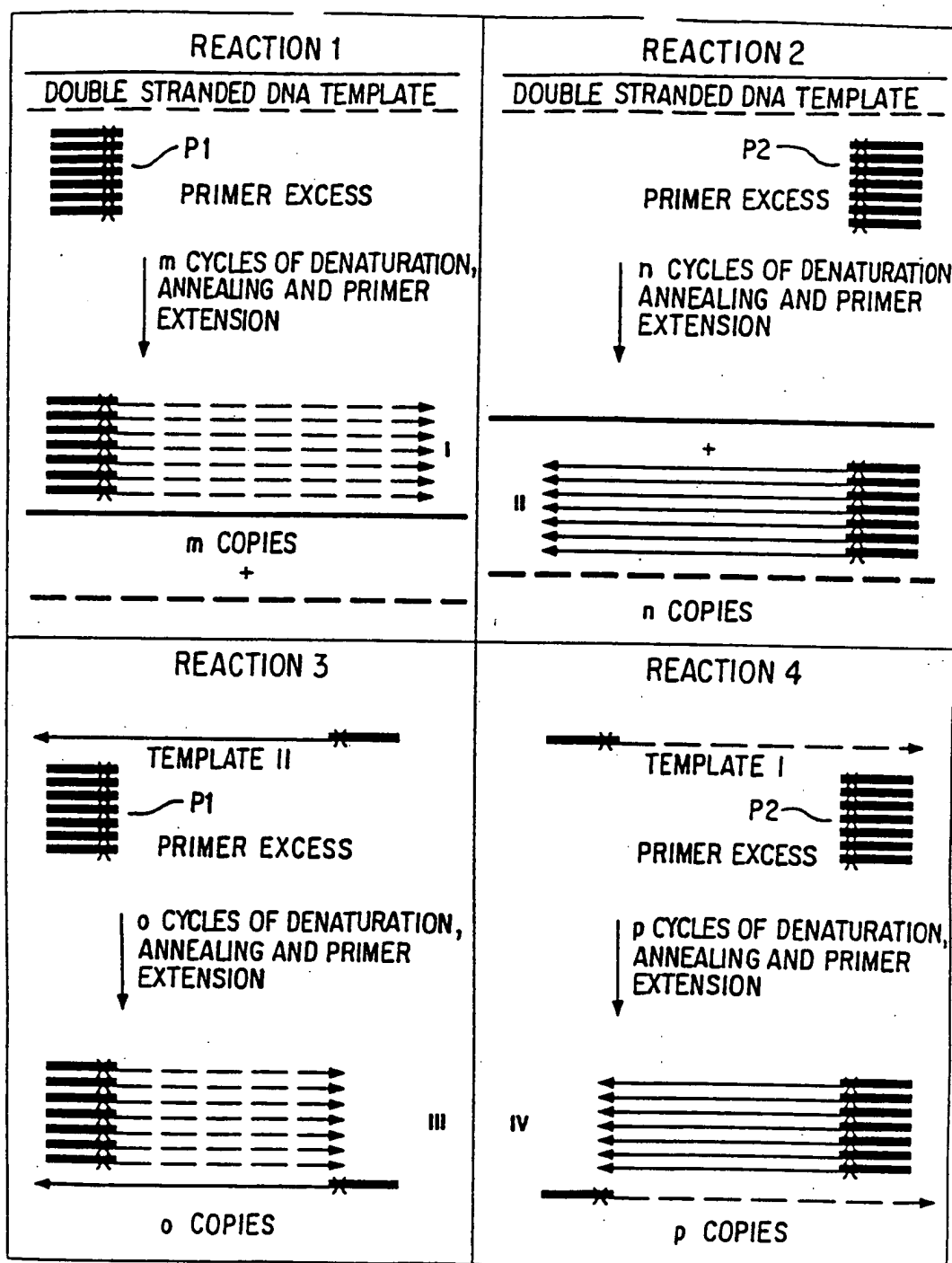


FIGURE 7

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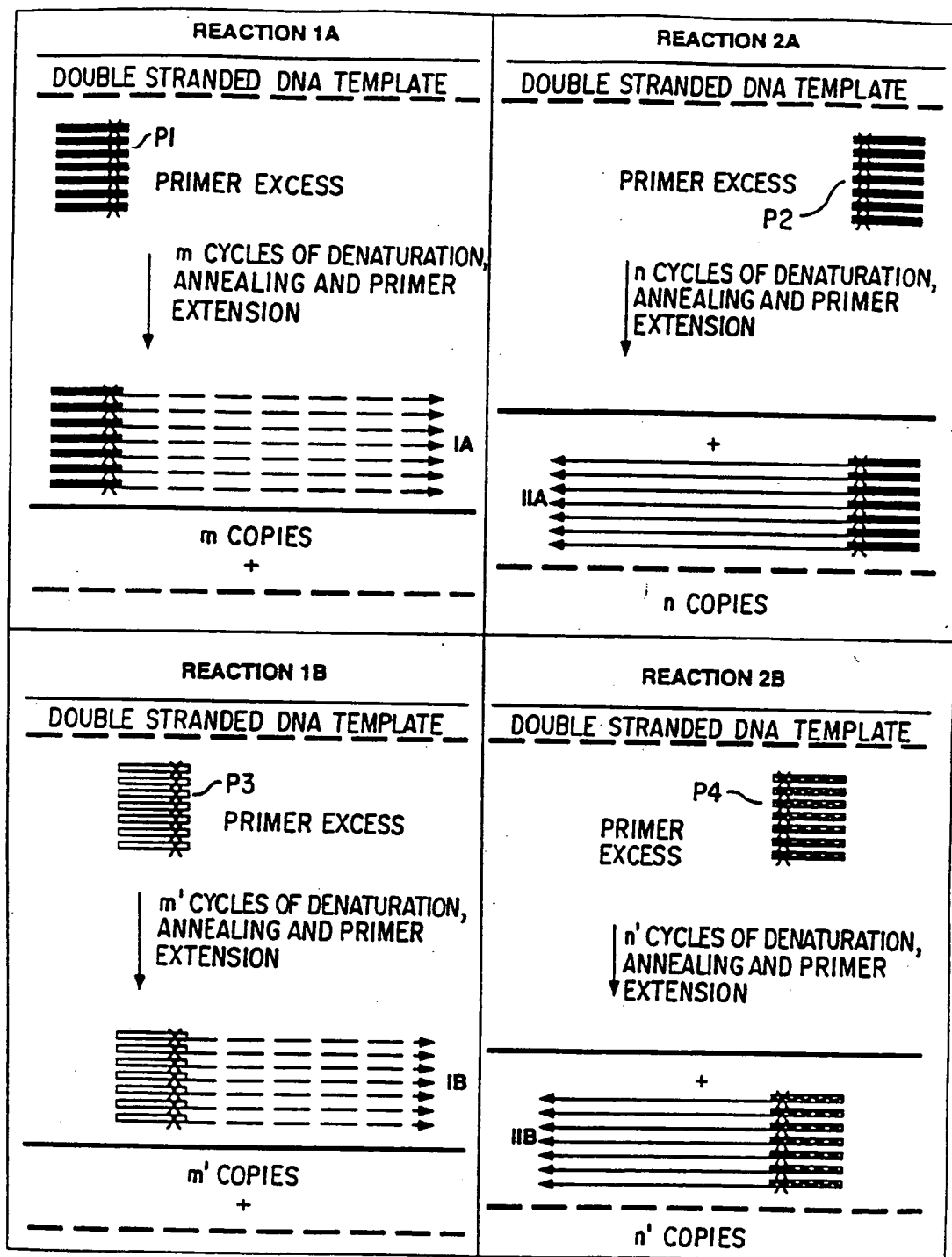


FIGURE 8

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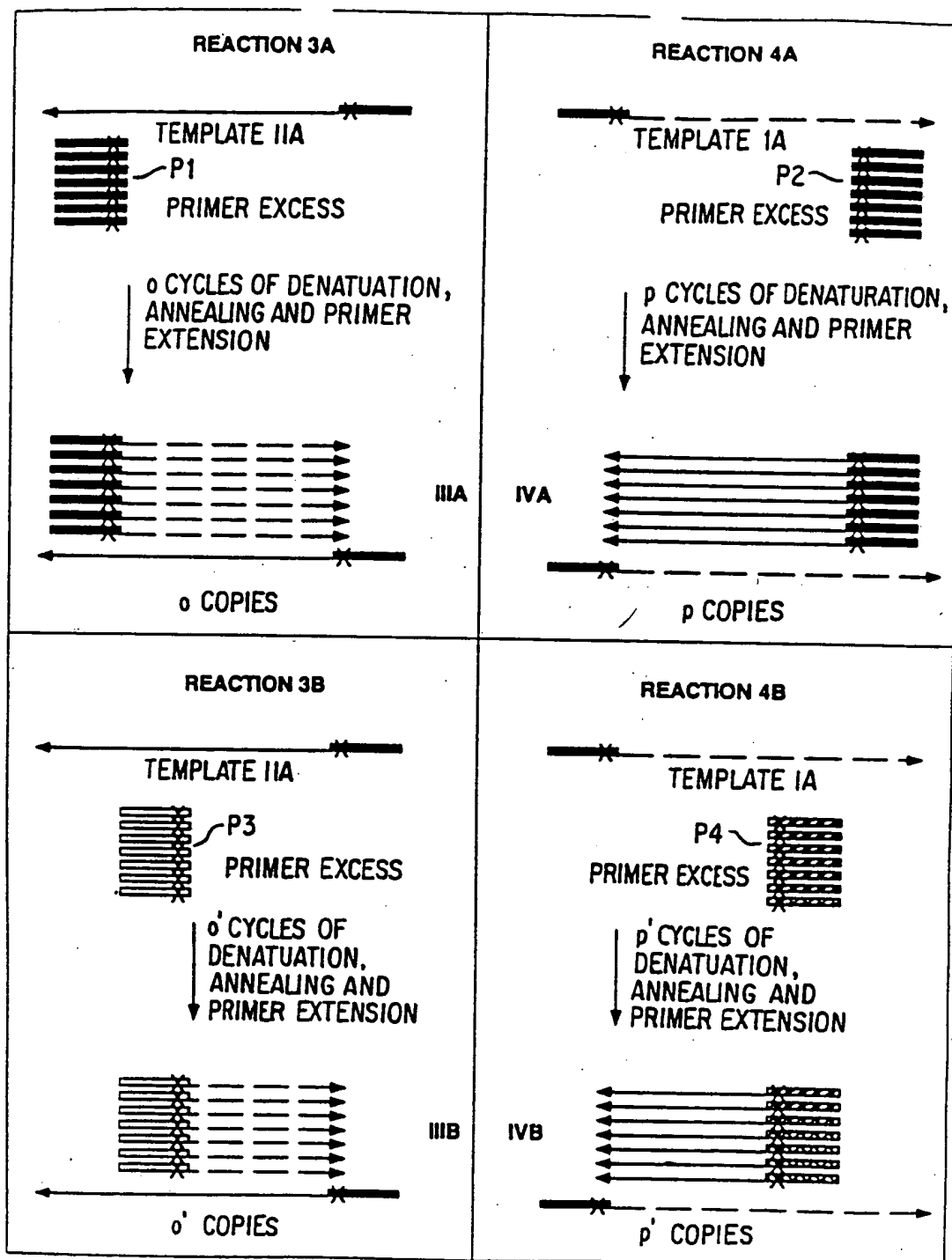


FIGURE 9

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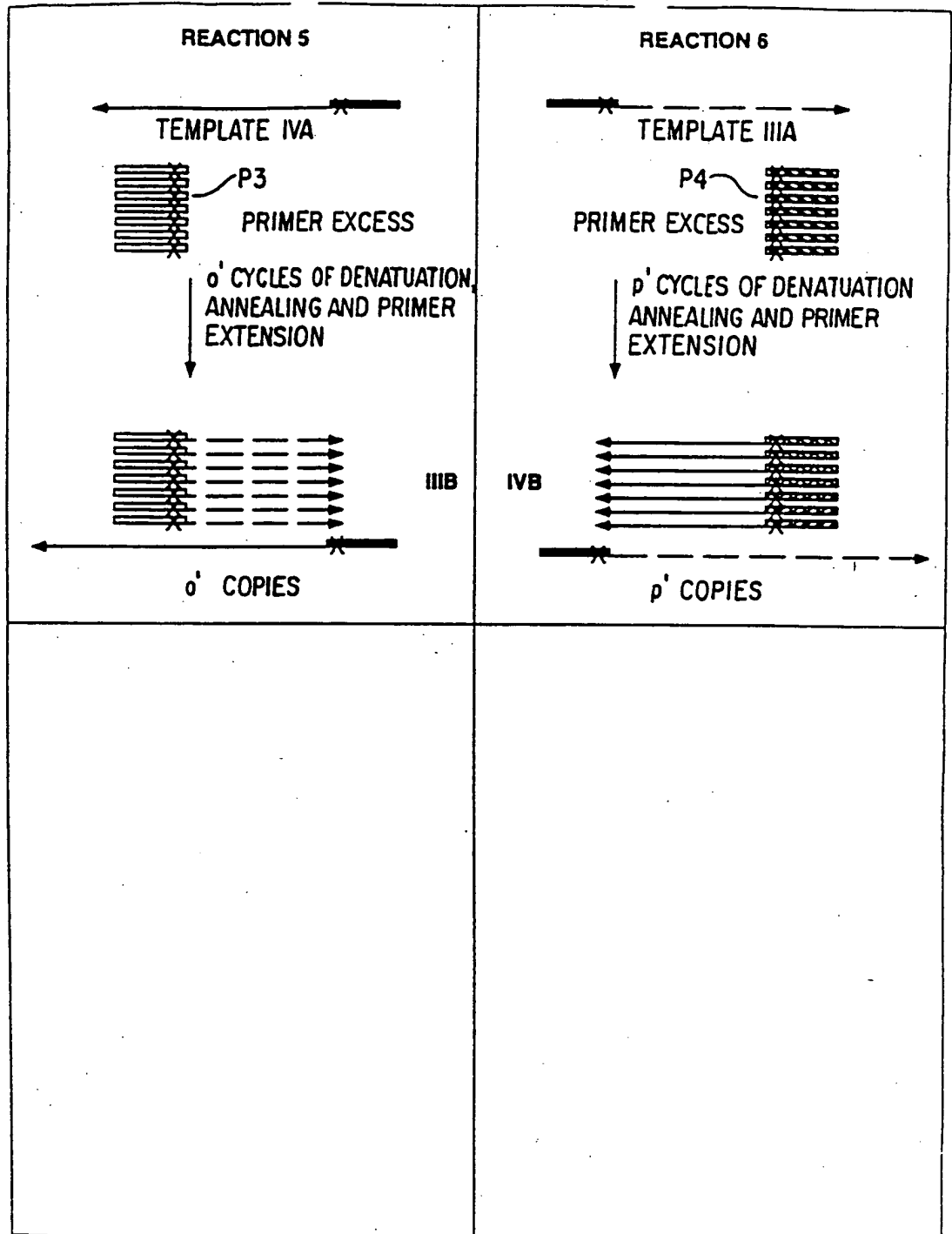
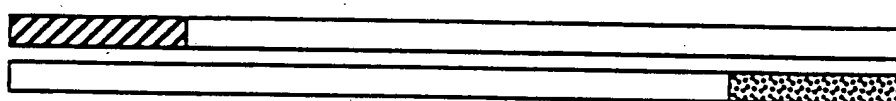


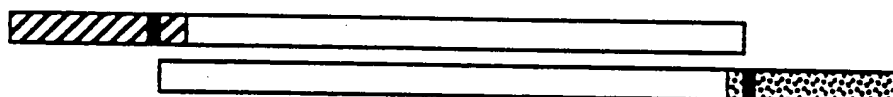
FIGURE 10

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- PRODUCT OF A PCR REACTION IS COMPLETELY DOUBLE STRANDED



- PRODUCTS OF AN LLA REACTION CAN BE ANNEALED TO FORM A DUPLEX WITH SINGLE STRANDED ENDS
- THIS PRODUCT IS SHORTER THAN THE CORRESPONDING PCR FRAGMENT

■ Non-replicable element

FIGURE 11

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CCCTACCCCTGTGGAGCCACACCTTAGGGTTGGCCAACTACTCCAGGAGCAGGGAGGGCAGGAGCCAGGGCTGGGCATAAAAGTCAGGGCAGAG 95

↑ b9p-5 35

Diagram illustrating the bpg-1 22 mutation, showing a bracket labeled "bpg-1 22" above a thick upward-pointing arrow.

CCATCTATTGCTTACATTTGCTTCTGACACAACTGTGTTCACTAGCAACCTCAAACAGACACCATGGTGACCTGACTCCTGAGGAGAAGTCTGC

CGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAAGTTGGTGGTGGGCCCTGGGCAGGTTCAAGGTTACAAGACAGGTTTAAGGAGA 285

CCCAATAGAAACTGGGCATGTGGAGACAGAGAAGACTCTGGGTTTCTGATAGGCACTGACTCTCTGCCTATTGGTCTATTTCCACCCCTTAG 380

bgp-2 22

GC T G C T G G T G G T C T A C C C T T G G A C C C A G A G G T T C T T T G A G T C C T T G G → 428

—bgp-4 35—

FIGURE 12

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : C12Q 1/70; C12P 19/34; C07H 21/02, 21/04

US CL : 435/6, 91.5; 536/24.33

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6, 91.5; 536/24.33

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

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C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X --- Y	INNIS et al., "PCR PROTOCOLS," published 1990 by ACADEMIC PRESS, INC (N.Y.), pages 189-195, see entire document.	1-6, 9-12, 14, 15, 18-20, 24, 25, 28, 31-33 7, 8, 13, 16, 17, 21-23, 26, 27, 29-30, 34- 42
Y	US, A, 4,683,195 (MULLIS ET AL.) 28 JULY 1987, see entire document.	7, 8, 13, 16, 17, 21-23, 26, 27, 29-30, 34- 42

☐ Further documents are listed in the continuation of Box C.
 ☐ See patent family annex.

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* L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	* A document member of the same patent family
* O document referring to an oral disclosure, use, exhibition or other means	
* P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

31 OCTOBER 1994

Date of mailing of the international search report

07 NOV 1994

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